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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/051,311A

DATE: 07/10/2002

TIME: 10:30:16

Input Set : A:\seqlist0652_2290001.txt
 Output Set: N:\CRF3\07102002\J051311A.raw

3 <110> APPLICANT: Boehringer Ingelheim International GmbH
 5 <120> TITLE OF INVENTION: Method for identifying compounds that modulate sister
 6 chromatid separation
 8 <130> FILE REFERENCE: 0652.2290001
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/051,311A
 C--> 11 <141> CURRENT FILING DATE: 2002-06-20
 13 <150> PRIOR APPLICATION NUMBER: EP 01 101 252.3
 14 <151> PRIOR FILING DATE: 2001-01-19
 16 <150> PRIOR APPLICATION NUMBER: US 60/297,440
 17 <151> PRIOR FILING DATE: 2001-06-13
 19 <160> NUMBER OF SEQ ID NOS: 13
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 6668
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: 5'UTR
 30 <222> LOCATION: (1)..(144)
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (145)..(6507)
 36 <220> FEATURE:
 37 <221> NAME/KEY: 3'UTR
 38 <222> LOCATION: (6508)..(6668)
 40 <400> SEQUENCE: 1
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 43 accttcagcc ctcttcctt cctccagttt gcttcattaa caatcttctc taattggct 120
 45 cttttccctt agctctccgg tttc atg agg agc ttc aaa aga gtc aac ttt 171
 46 Met Arg Ser Phe Lys Arg Val Asn Phe
 47 1 5
 49 ggg act ctg cta agc agc cag aag gag gct gaa gag ttg ctg ccc gac 219
 50 Gly Thr Leu Leu Ser Ser Gln Lys Glu Ala Glu Glu Leu Leu Pro Asp
 51 10 15 20 25
 53 ttg aag gag ttc ctg tcc aac cct cca gct ggt ttt ccc agc agc cga 267
 54 Leu Lys Glu Phe Leu Ser Asn Pro Pro Ala Gly Phe Pro Ser Ser Arg
 55 30 35 40
 57 tct gat gct gag agg aga caa gct tgt gat gcc atc ctg agg gct tgc 315
 58 Ser Asp Ala Glu Arg Arg Gln Ala Cys Asp Ala Ile Leu Arg Ala Cys
 59 45 50 55
 61 aac cag cag ctg act gct aag cta gct tgc cct agg cat ctg ggg agc 363
 62 Asn Gln Gln Leu Thr Ala Lys Leu Ala Cys Pro Arg His Leu Gly Ser
 63 60 65 70

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65	ctg	ctg	gag	ctg	gca	gag	ctg	gcc	tgt	gat	ggc	tac	tta	gtg	tct	acc	411
66	Leu	Leu	Glu	Leu	Ala	Glu	Leu	Ala	Cys	Asp	Gly	Tyr	Leu	Val	Ser	Thr	
67	75				80								85				
70	cca	cag	cgt	cct	ccc	ctc	tac	ctg	gaa	cga	att	ctc	ttt	gtc	tta	ctg	459
71	Pro	Gln	Arg	Pro	Pro	Leu	Tyr	Leu	Glu	Arg	Ile	Leu	Phe	Val	Leu	Leu	
72	90				95						100				105		
74	cgg	aat	gct	gct	gca	caa	gga	agc	cca	gag	gtc	aca	ctc	cgc	ctt	gct	507
75	Arg	Asn	Ala	Ala	Ala	Gln	Gly	Ser	Pro	Glu	Val	Thr	Leu	Arg	Leu	Ala	
76					110						115				120		
78	cag	ccc	ctc	cat	gcc	tgc	ttg	gtg	cag	tgc	tct	cgc	gag	gct	gct	ccc	555
79	Gln	Pro	Leu	His	Ala	Cys	Leu	Val	Gln	Cys	Ser	Arg	Glu	Ala	Ala	Pro	
80					125					130				135			
82	cag	gac	tat	gag	gcc	gtg	gct	cg	ggc	agc	ttt	tct	ctg	ctt	tgg	aag	603
83	Gln	Asp	Tyr	Glu	Ala	Val	Ala	Arg	Gly	Ser	Phe	Ser	Leu	Leu	Trp	Lys	
84					140					145				150			
86	ggg	gca	gaa	gcc	ctg	ttg	gaa	cgg	cga	gct	gca	ttt	gca	gct	cgg	ctg	651
87	Gly	Ala	Glu	Ala	Leu	Leu	Glu	Arg	Arg	Ala	Ala	Phe	Ala	Ala	Arg	Leu	
88					155					160				165			
90	aag	gcc	ttg	agc	ttc	cta	gta	ctc	ttg	gag	gat	gaa	agt	acc	cct	tgt	699
91	Lys	Ala	Leu	Ser	Phe	Leu	Val	Leu	Leu	Glu	Asp	Glu	Ser	Thr	Pro	Cys	
92	170				175					180				185			
94	gag	gtt	cct	cac	ttt	gtc	tct	cca	aca	gcc	tgt	cga	gcg	gta	gct	gcc	747
95	Glu	Val	Pro	His	Phe	Ala	Ser	Pro	Thr	Ala	Cys	Arg	Ala	Val	Ala	Ala	
96					190					195				200			
98	cat	cag	cta	ttt	gat	gcc	agt	ggc	cat	gtt	cta	aat	gaa	gca	gat	gct	795
99	His	Gln	Leu	Phe	Asp	Ala	Ser	Gly	His	Gly	Leu	Asn	Glu	Ala	Asp	Ala	
100					205					210				215			
102	gat	ttc	cta	gat	gac	ctg	ctc	agg	cac	gtg	atc	aga	gcc	ttg	gtg		843
103	Asp	Phe	Leu	Asp	Asp	Leu	Leu	Ser	Arg	His	Val	Ile	Arg	Ala	Leu	Val	
104					220					225				230			
106	ggt	gag	aga	ggg	agc	tct	tct	ggg	ctt	ctt	tct	ccc	cag	agg	gcc	ctc	891
107	Gly	Glu	Arg	Gly	Ser	Ser	Ser	Gly	Leu	Leu	Ser	Pro	Gln	Arg	Ala	Leu	
108					235					240				245			
110	tgc	ctc	ttg	gag	ctc	acc	ttg	gaa	cac	tgc	cgt	ttt	tgc	tgg	agc		939
111	Cys	Leu	Leu	Glu	Leu	Thr	Leu	Glu	His	Cys	Arg	Arg	Phe	Cys	Trp	Ser	
112	250				255					260				265			
114	cgc	cac	cat	gac	aaa	gcc	atc	agc	gca	gtg	gag	aag	gct	cac	agt	tac	987
115	Arg	His	His	Asp	Lys	Ala	Ile	Ser	Ala	Val	Glu	Lys	Ala	His	Ser	Tyr	
116					270					275				280			
118	cta	agg	aac	acc	aat	cta	gcc	cct	agc	ttt	cag	cta	tgt	cag	ctg	ggg	1035
119	Leu	Arg	Asn	Thr	Asn	Leu	Ala	Pro	Ser	Leu	Gln	Leu	Cys	Gln	Leu	Gly	
120					285					290				295			
122	gtt	aag	ctg	ctg	cag	gtt	ggg	gag	gaa	gga	cct	cag	gca	gtg	gcc	aag	1083
123	Val	Lys	Leu	Leu	Gln	Val	Gly	Glu	Glu	Gly	Pro	Gln	Ala	Val	Ala	Lys	
124					300					305				310			
126	ctt	ctg	atc	aag	gca	tca	gct	gtc	ctg	agc	aag	agt	atg	gag	gca	cca	1131
127	Leu	Leu	Ile	Lys	Ala	Ser	Ala	Val	Leu	Ser	Lys	Ser	Met	Glu	Ala	Pro	
128					315					320				325			
130	tca	ccc	cca	ctt	cg	gca	ttg	tat	gag	agc	tgc	cag	ttc	tcc	ttt	tca	1179

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131	Ser	Pro	Pro	Leu	Arg	Ala	Leu	Tyr	Glu	Ser	Cys	Gln	Phe	Phe	Leu	Ser	
132	330					335					340					345	
134	ggc	ctg	gaa	cga	ggc	acc	aag	agg	cgc	tat	aga	ctt	gat	gcc	att	ctg	
135	Gly	Leu	Glu	Arg	Gly	Thr	Lys	Arg	Arg	Tyr	Arg	Leu	Asp	Ala	Ile	Leu	
136						350					355					360	
138	agc	ctc	ttt	gct	ttt	ctt	gga	ggg	tac	tgc	tct	ctt	ctg	cag	cag	ctg	
139	Ser	Leu	Phe	Ala	Phe	Leu	Gly	Gly	Tyr	Cys	Ser	Leu	Leu	Gln	Gln	Leu	
140						365					370					375	
142	cgg	gat	gat	ggt	gtg	tat	ggg	ggc	tcc	tcc	aag	caa	cag	cag	tct	ttt	
143	Arg	Asp	Asp	Gly	Val	Tyr	Gly	Gly	Ser	Ser	Lys	Gln	Gln	Gln	Ser	Phe	
144						380					385					390	
146	ctt	cag	atg	tac	ttt	cag	gga	ctt	cac	ctc	tac	act	gtg	gtg	gtt	tat	
147	Leu	Gln	Met	Tyr	Phe	Gln	Gly	Leu	His	Leu	Tyr	Thr	Val	Val	Val	Tyr	
148						395					400					405	
150	gac	ttt	gcc	caa	ggc	tgt	cag	ata	gtt	gat	ttg	gtc	gac	ctg	acc	caa	
151	Asp	Phe	Ala	Gln	Gly	Cys	Gln	Ile	Val	Asp	Leu	Ala	Asp	Leu	Thr	Gln	
152	410						415					420				425	
154	cta	gtg	gac	agt	tgt	aaa	tct	acc	gtt	gtc	tgg	atg	ctg	gag	gcc	tta	
155	Leu	Val	Asp	Ser	Cys	Lys	Ser	Thr	Val	Val	Val	Trp	Met	Leu	Glu	Ala	Leu
156						430					435					440	
158	gag	ggc	ctg	tcg	ggc	caa	gag	ctg	acg	gac	cac	atg	ggg	atg	acc	gtc	
159	Glu	Gly	Leu	Ser	Gly	Gln	Glu	Leu	Thr	Asp	His	Met	Gly	Met	Thr	Ala	
160						445					450					455	
162	tct	tac	acc	agt	aat	ttg	gcc	tac	agc	tcc	tat	agt	cac	aag	ctc	tat	
163	Ser	Tyr	Thr	Ser	Asn	Leu	Ala	Tyr	Ser	Phe	Tyr	Ser	His	Lys	Leu	Tyr	
164						460					465					470	
166	gcc	gag	gcc	tgt	gcc	atc	tct	gag	ccg	ctc	tgt	cag	cac	ctg	ggt	ttg	
167	Ala	Glu	Ala	Cys	Ala	Ile	Ser	Glu	Pro	Leu	Cys	Gln	His	Leu	Gly	Leu	
168						475					480					485	
170	gtg	aag	cca	ggc	act	tat	ccc	gag	gtg	cct	cct	gag	aag	ttg	cac	agg	
171	Val	Lys	Pro	Gly	Thr	Tyr	Pro	Glu	Val	Pro	Pro	Glu	Lys	Leu	His	Arg	
172	490						495					500				505	
174	tgc	ttc	cgg	cta	caa	gta	gag	agt	ttg	aag	aaa	ctg	ggt	aaa	cag	gcc	
175	Cys	Phe	Arg	Leu	Gln	Val	Glu	Ser	Leu	Lys	Lys	Leu	Gly	Lys	Gln	Ala	
176						510					515					520	
178	cag	ggc	tgc	aag	atg	gtg	att	ttg	tgg	ctg	gca	gcc	ctg	caa	ccc	tgt	
179	Gln	Gly	Cys	Lys	Met	Val	Ile	Leu	Trp	Leu	Ala	Ala	Leu	Gln	Pro	Cys	
180						525					530					535	
182	agc	cct	gaa	cac	atg	gct	gag	cca	gtc	act	ttc	tgg	gtt	cg	gtc	aag	
183	Ser	Pro	Glu	His	Met	Ala	Glu	Pro	Val	Thr	Phe	Trp	Val	Arg	Val	Lys	
184						540					545					550	
186	atg	gat	gct	gcc	agg	gct	gga	gac	aag	gag	cta	cag	cta	aag	act	ctg	
187	Met	Asp	Ala	Ala	Arg	Ala	Gly	Asp	Lys	Glu	Leu	Gln	Leu	Lys	Thr	Leu	
188						555					560					565	
190	cga	gac	agc	ctc	agt	ggc	tgg	gac	ccg	gag	acc	ctg	gcc	ctc	ctg	ctg	
192	Arg	Asp	Ser	Leu	Ser	Gly	Trp	Asp	Pro	Glu	Thr	Leu	Ala	Leu	Leu	Leu	
193	570						575					580				585	
196	agg	gag	gag	ctg	cag	gcc	tac	aag	gct	gtg	cg	gcc	gac	act	gga	cag	
197	Arg	Glu	Glu	Leu	Gln	Ala	Tyr	Lys	Ala	Val	Arg	Ala	Asp	Thr	Gly	Gln	

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201	Glu Arg Phe Asn Ile Ile Cys Asp Leu Leu Glu Leu Ser Pro Glu Glu			
202	605	610	615	
204	aca cca gcc ggg gcc tgg gca cga gcc acc cac ctg gta gaa ctg gct			2043
205	Thr Pro Ala Gly Ala Trp Ala Arg Ala Thr His Leu Val Glu Leu Ala			
206	620	625	630	
208	cag gtg ctc tgc tac cac gac ttt acg cag cag acc aac tgc tct gct			2091
209	Gln Val Leu Cys Tyr His Asp Phe Thr Gln Gln Thr Asn Cys Ser Ala			
210	635	640	645	
212	ctg gat gct atc cgg gaa gcc ctg cag ctt ctg gac tct gtg agg cct			2139
213	Leu Asp Ala Ile Arg Glu Ala Leu Gln Leu Leu Asp Ser Val Arg Pro			
214	650	655	660	665
216	gag gcc cag gcc aga gat cag ctt ctg gac gat aaa gca cag gcc ttg			2187
217	Glu Ala Gln Ala Arg Asp Gln Leu Leu Asp Asp Lys Ala Gln Ala Leu			
218	670	675	680	
220	ctg tgg ctt tac atc tgt act ctg gaa gcc aaa ata cag gaa ggt atc			2235
221	Leu Trp Leu Tyr Ile Cys Thr Leu Glu Ala Lys Ile Gln Glu Gly Ile			
222	685	690	695	
224	gag cgg gat cgg aga gcc cag gcc cct ggt aac ttg gag gaa ttt gaa			2283
225	Glu Arg Asp Arg Arg Ala Gln Ala Pro Gly Asn Leu Glu Glu Phe Glu			
226	700	705	710	
228	gtc aat gac ctg aac tat gaa gat aaa ctc cag gaa gat cgt ttc cta			2331
229	Val Asn Asp Leu Asn Tyr Glu Asp Lys Leu Gln Glu Asp Arg Phe Leu			
230	715	720	725	
232	tac agt aac att gcc ttc aac ctg gct gca gat gct gct cag tcc aaa			2379
233	Tyr Ser Asn Ile Ala Phe Asn Leu Ala Ala Asp Ala Ala Gln Ser Lys			
234	730	735	740	745
236	tgc ctg gac caa gcc ctg gcc ctg tgg aag gag ctg ctt aca aag ggg			2427
237	Cys Leu Asp Gln Ala Leu Ala Leu Trp Lys Glu Leu Leu Thr Lys Gly			
238	750	755	760	
240	cag gcc cca gct gta cgg tgt ctc cag cag aca gca gcc tca ctg cag			2475
241	Gln Ala Pro Ala Val Arg Cys Leu Gln Gln Thr Ala Ala Ser Leu Gln			
242	765	770	775	
244	atc cta gca gcc ctc tac cag ctg gtg gca aag ccc atg cag gct ctg			2523
245	Ile Leu Ala Ala Leu Tyr Gln Leu Val Ala Lys Pro Met Gln Ala Leu			
246	780	785	790	
248	gag gtc ctc ctg cta cgg att gtc tct gag aga ctg aag gac cac			2571
249	Glu Val Leu Leu Leu Arg Ile Val Ser Glu Arg Leu Lys Asp His			
250	795	800	805	
252	tcg aag gca gct ggc tcc tcc tgc cac atc acc cag ctc ctc ctg acc			2619
253	Ser Lys Ala Ala Gly Ser Ser Cys His Ile Thr Gln Leu Leu Thr			
254	810	815	820	825
257	ctc ggc tgt ccc agc tat gcc cag tta cac ctg gaa gag gca gca tcg			2667
258	Leu Gly Cys Pro Ser Tyr Ala Gln Leu His Leu Glu Glu Ala Ala Ser			
259	830	835	840	
261	agc ctg aag cat ctc gat cag act act gac aca tac ctg ctc ctt tcc			2715
262	Ser Leu Lys His Leu Asp Gln Thr Thr Asp Thr Tyr Leu Leu Ser			
263	845	850	855	

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266	Leu	Thr	Cys	Asp	Leu	Leu	Arg	Ser	Gln	Leu	Tyr	Trp	Thr	His	Gln	Lys		
267	860															870		
269	gtg	acc	aag	ggt	gtc	tct	ctg	ctg	tct	gtg	ctt	cgg	gat	cct	gcc	2811		
270	Val	Thr	Lys	Gly	Val	Ser	Leu	Leu	Leu	Ser	Val	Leu	Arg	Asp	Pro	Ala		
271	875															885		
273	ctc	cag	aag	tcc	tcc	aag	gct	tgg	tac	ttg	ctg	cgt	gtc	cag	gtc	ctg	2859	
274	Leu	Gln	Lys	Ser	Ser	Lys	Ala	Trp	Tyr	Leu	Leu	Arg	Val	Gln	Val	Leu		
275	890															905		
277	cag	ctg	gtg	gca	gct	tac	ctt	agc	ctc	ccg	tca	aac	aac	ctc	tca	cac	2907	
278	Gln	Leu	Val	Ala	Ala	Tyr	Leu	Ser	Leu	Pro	Ser	Asn	Asn	Leu	Ser	His		
279	910															920		
281	tcc	ctg	tgg	gag	cag	ctc	tgt	gcc	caa	gca	tgg	cag	aca	cct	gag	ata	2955	
282	Ser	Leu	Trp	Glu	Gln	Leu	Cys	Ala	Gln	Gly	Trp	Gln	Thr	Pro	Glu	Ile		
283	925															935		
285	gct	ctc	ata	gac	tcc	cat	aag	ctc	ctc	cga	agc	atc	atc	ctc	ctg	ctg	3003	
286	Ala	Leu	Ile	Asp	Ser	His	Lys	Leu	Leu	Arg	Ser	Ile	Ile	Leu	Leu	Leu		
287	940															950		
289	atg	ggc	agt	gac	att	ctc	tca	act	cag	aaa	gca	gct	gtg	gag	aca	tcg	3051	
290	Met	Gly	Ser	Asp	Ile	Leu	Ser	Thr	Gln	Lys	Ala	Ala	Val	Glu	Thr	Ser		
291	955															965		
293	ttt	ttg	gac	tat	ggt	gaa	aat	ctg	gta	caa	aaa	tgg	cag	gtt	ctt	tca	3099	
294	Phe	Leu	Asp	Tyr	Gly	Glu	Asn	Leu	Val	Gln	Lys	Trp	Gln	Val	Leu	Ser		
295	970															985		
297	gag	gtg	ctg	agc	tgc	tca	gag	aag	ctg	gtc	tgc	cac	ctg	ggc	cgc	ctg	3147	
298	Glu	Val	Leu	Ser	Cys	Ser	Glu	Lys	Leu	Val	Cys	His	Leu	Gly	Arg	Leu		
299	990															1000		
301	ggt	agt	gtg	agt	gaa	gcc	aag	gcc	ttt	tgc	ttg	gag	gcc	cta	aaa	ctt	3195	
302	Gly	Ser	Val	Ser	Glu	Ala	Lys	Ala	Phe	Cys	Leu	Glu	Ala	Leu	Lys	Leu		
303	1005															1015		
305	aca	aca	aag	ctg	cag	ata	cca	cgc	cag	tgt	gcc	ctg	ttc	ctg	gtg	ctg	3243	
306	Thr	Thr	Lys	Leu	Gln	Ile	Pro	Arg	Gln	Cys	Ala	Leu	Phe	Leu	Val	Leu		
307	1020															1030		
309	aag	ggc	gag	ctg	gag	ctg	gcc	cgc	aat	gac	att	gtc	tgt	cag	tcg	3291		
310	Lys	Gly	Glu	Leu	Glu	Leu	Ala	Arg	Asn	Asp	Ile	Asp	Leu	Cys	Gln	Ser		
311	1035															1045		
313	gac	ctg	cag	cag	gtt	ctg	ttc	ttg	ctt	gag	tct	tgc	aca	gag	ttt	ggt	3339	
314	Asp	Leu	Gln	Gln	Val	Leu	Phe	Leu	Leu	Glu	Ser	Cys	Thr	Glu	Phe	Gly		
315	1050															1065		
318	ggg	gtg	act	cag	cac	ctg	gac	tct	gtg	aag	aag	gtc	cac	ctg	cag	aag	3387	
319	Gly	Val	Thr	Gln	His	Leu	Asp	Ser	Val	Lys	Lys	Val	His	Leu	Gln	Lys		
320	1070															1080		
322	ggg	aag	cag	cag	gcc	cag	gtc	ccc	tgt	cct	cca	cag	ctc	cca	gag	gag	3435	
323	Gly	Lys	Gln	Gln	Ala	Gln	Val	Pro	Cys	Pro	Pro	Gln	Leu	Pro	Glu	Glu		
324	1085															1095		
326	gag	ctc	ttc	cta	aga	ggc	cct	gct	cta	gag	ctg	gtg	gcc	act	gtg	gcc	3483	
327	Glu	Leu	Phe	Leu	Arg	Gly	Pro	Ala	Leu	Glu	Leu	Val	Ala	Thr	Val	Ala		
328	1100															1110		
330	aag	gag	cct	ggc	ccc	ata	gca	cct	tct	aca	aac	tcc	tcc	cca	gtc	ttg	3531	

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1165 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13